RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/531,844 A_____

Source: _____ IFW/6 _____

Date Processed by STIC: _____ 10/06/2006 _____

ENTERED

IFW16

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  3 <110> APPLICANT: Jahic, Haris
  4         Kern, Gunther
  6 <120> TITLE OF INVENTION: Screening Assay to Identify Inhibitors of the MurD Enzyme
using
  7         an Activator-Independent MurD enzyme
  9 <130> FILE REFERENCE: RE: 100874-1P US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/531,844A
C--> 11 <141> CURRENT FILING DATE: 2005-04-18
  11 <150> PRIOR APPLICATION NUMBER: GB 0224997.7
  12 <151> PRIOR FILING DATE: 2002-10-26
  14 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/004592
  15 <151> PRIOR FILING DATE: 2003-10-23
  17 <160> NUMBER OF SEQ ID NOS: 4
  19 <170> SOFTWARE: PatentIn version 3.3
  21 <210> SEQ ID NO: 1
  22 <211> LENGTH: 438
  23 <212> TYPE: PRT
  24 <213> ORGANISM: Escherichia coli
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  33             20                  25                  30
  36 Arg Val Met Asp Thr Arg Met Thr Pro Pro Gly Leu Asp Lys Leu Pro
  37         35                  40                  45
  40 Glu Ala Val Glu Arg His Thr Gly Ser Leu Asn Asp Glu Trp Leu Met
  41     50                  55                  60
  44 Ala Ala Asp Leu Ile Val Ala Ser Pro Gly Ile Ala Leu Ala His Pro
  45 65                  70                  75                  80
  48 Ser Leu Ser Ala Ala Ala Asp Ala Gly Ile Glu Ile Val Gly Asp Ile
  49             85                  90                  95
  52 Glu Leu Phe Cys Arg Glu Ala Gln Ala Pro Ile Val Ala Ile Thr Gly
  53             100                 105                 110
  56 Ser Asn Gly Lys Ser Thr Val Thr Thr Leu Val Gly Glu Met Ala Lys
  57         115                 120                 125
  60 Ala Ala Gly Val Asn Val Gly Val Gly Gly Asn Ile Gly Leu Pro Ala
  61     130                 135                 140
  64 Leu Met Leu Leu Asp Asp Glu Cys Glu Leu Tyr Val Leu Glu Leu Ser
  65 145                 150                 155                 160
  68 Ser Phe Gln Leu Glu Thr Thr Ser Ser Leu Gln Ala Val Ala Ala Thr
  69             165                 170                 175
  72 Ile Leu Asn Val Thr Glu Asp His Met Asp Arg Tyr Pro Phe Gly Leu
  73             180                 185                 190
  76 Gln Gln Tyr Arg Ala Ala Lys Leu Arg Ile Tyr Glu Asn Ala Lys Val
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77           195                200                205
80 Cys Val Val Asn Ala Asp Asp Ala Leu Thr Met Pro Ile Arg Gly Ala
81     210                215                220
84 Asp Glu Arg Cys Val Ser Phe Gly Val Asn Met Gly Asp Tyr His Leu
85 225                230                235                240
88 Asn His Gln Gln Gly Glu Thr Trp Leu Arg Val Lys Gly Glu Lys Val
89                245                250                255
92 Leu Asn Val Lys Glu Met Lys Leu Ser Gly Gln His Asn Tyr Thr Asn
93                260                265                270
96 Ala Leu Ala Ala Leu Ala Leu Ala Asp Ala Ala Gly Leu Pro Arg Ala
97          275                280                285
100 Ser Ser Leu Lys Ala Leu Thr Thr Phe Thr Gly Leu Pro His Arg Phe
101     290                295                300
104 Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys
105 305                310                315                320
108 Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val
109                325                330                335
112 Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp
113          340                345                350
116 Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr
117          355                360                365
120 Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val
121     370                375                380
124 Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro
125 385                390                395                400
128 Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser
129                405                410                415
132 Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg
133          420                425                430
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140 <210> SEQ ID NO: 2
141 <211> LENGTH: 456
142 <212> TYPE: PRT
143 <213> ORGANISM: Escherichia faecalis
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151 Leu Ala Lys Ser Gly Val Ser Ala Ala Lys Leu Leu His Glu Leu Gly
152          20                25                30
155 Ala Leu Val Thr Val Asn Asp Ala Lys Gln Phe Asp Gln Asn Pro Asp
156          35                40                45
159 Ala Gln Asp Leu Leu Thr Leu Gly Ile Arg Val Val Thr Gly Gly His
160     50                55                60
163 Pro Ile Glu Leu Leu Asp Glu Glu Phe Glu Leu Ile Val Lys Asn Pro
164 65                70                75                80
167 Gly Ile Leu Tyr Thr Asn Pro Leu Val Ala Glu Ala Leu Thr Arg Lys
168          85                90                95
171 Ile Pro Ile Ile Thr Glu Val Glu Leu Ala Gly Gln Ile Ala Glu Cys
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172               100               105               110
175 Pro Ile Val Gly Ile Thr Gly Thr Asn Gly Lys Thr Thr Thr Thr
176         115               120               125
179 Met Ile Gly Leu Leu Leu Asn Ala Asp Arg Thr Ala Gly Glu Ala Arg
180         130               135               140
183 Leu Ala Gly Asn Ile Gly Phe Pro Ala Ser Thr Val Ala Gln Glu Ala
184 145               150               155               160
187 Thr Ala Lys Asp Asp Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met
188               165               170               175
191 Gly Ile Glu Thr Phe His Pro Gln Ile Ala Val Ile Thr Asn Ile Phe
192               180               185               190
195 Glu Ala His Leu Asp Tyr His Gly Ser Arg Lys Glu Tyr Val Ala Ala
196         195               200               205
199 Lys Trp Ala Ile Gln Lys Asn Met Thr Ala Glu Asp Thr Leu Ile Leu
200         210               215               220
203 Asn Trp Asn Gln Val Glu Leu Gln Thr Leu Ala Lys Thr Thr Ala Ala
204 225               230               235               240
207 Asn Val Leu Pro Phe Ser Thr Lys Glu Ala Val Glu Gly Ala Tyr Leu
208               245               250               255
211 Leu Asp Gly Lys Leu Tyr Phe Asn Glu Glu Tyr Ile Met Pro Ala Asp
212         260               265               270
215 Glu Leu Gly Ile Pro Gly Ser His Asn Ile Glu Asn Ala Leu Ala Ala
216         275               280               285
219 Ile Cys Val Pro Lys Leu Lys Asn Val Ser Asn Ala Gln Ile Lys Gln
220         290               295               300
223 Ser Leu Thr Asn Phe Ser Gly Val Pro His Arg Thr Gln Phe Val Gly
224 305               310               315               320
227 Glu Val Gln Gln Arg Arg Phe Tyr Asn Asp Ser Lys Ala Thr Asn Phe
228               325               330               335
231 Leu Ala Thr Glu Met Ala Leu Ser Gly Phe Asp Asn Gln Lys Leu Leu
232         340               345               350
235 Leu Leu Ala Gly Gly Leu Asp Arg Gly Asn Ser Phe Asp Glu Leu Val
236         355               360               365
239 Pro Ala Leu Leu Gly Leu Lys Ala Ile Val Leu Phe Gly Glu Thr Lys
240         370               375               380
243 Lys Lys Leu Ala Glu Ala Ala Lys Lys Pro Asn Ile Glu Thr Ile Leu
244 385               390               395               400
247 Phe Ala Glu Asn Val Gln Thr Ala Val Thr Ile Ala Phe Asp Tyr Ser
248               405               410               415
251 Glu Lys Asp Asp Thr Ile Leu Leu Ser Pro Ala Cys Ala Ser Trp Asp
252         420               425               430
255 Gln Tyr Pro Asn Phe Glu Val Arg Gly Glu Ala Phe Met Gln Ala Val
256         435               440               445
259 Gln Gln Leu Lys Glu Ser Glu Met
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264 <211> LENGTH: 448
265 <212> TYPE: PRT
266 <213> ORGANISM: Pseudomonas aeruginosa
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278 Phe Ala Val Val Asp Thr Arg Glu Asn Pro Pro Glu Leu Ala Thr Leu
279             35                  40                  45
282 Arg Ala Gln Tyr Pro Gln Val Glu Val Arg Cys Gly Glu Leu Asp Ala
283     50                  55                  60
286 Glu Phe Leu Cys Ser Ala Arg Glu Leu Tyr Val Ser Pro Gly Leu Ser
287 65                  70                  75                  80
290 Leu Arg Thr Pro Ala Leu Val Gln Ala Ala Ala Lys Gly Val Arg Ile
291             85                  90                  95
294 Ser Gly Asp Ile Asp Leu Phe Ala Arg Glu Ala Lys Ala Pro Ile Val
295             100                 105                 110
298 Ala Ile Thr Gly Ser Asn Ala Lys Ser Thr Val Thr Thr Leu Val Gly
299             115                 120                 125
302 Glu Met Ala Val Ala Ala Asp Lys Arg Val Ala Val Gly Gly Asn Leu
303     130                 135                 140
306 Gly Thr Pro Ala Leu Asp Leu Leu Ala Asp Asp Ile Glu Leu Tyr Val
307 145                 150                 155                 160
310 Leu Glu Leu Ser Ser Phe Gln Leu Glu Thr Cys Asp Arg Leu Asn Ala
311             165                 170                 175
314 Glu Val Ala Thr Val Leu Asn Val Ser Glu Asp His Met Asp Arg Tyr
315             180                 185                 190
318 Asp Gly Met Ala Asp Tyr His Leu Ala Lys His Arg Ile Phe Arg Gly
319             195                 200                 .205
322 Ala Arg Gln Val Val Val Asn Arg Ala Asp Ala Leu Thr Arg Pro Leu
323     210                 215                 220
326 Ile Ala Asp Thr Val Pro Cys Trp Ser Phe Gly Leu Asn Lys Pro Asp
327 225                 230                 235                 240
330 Phe Lys Ala Phe Gly Leu Ile Glu Glu Asp Gly Gln Lys Trp Leu Ala
331             245                 250                 255
334 Phe Gln Phe Asp Lys Leu Leu Pro Val Gly Glu Leu Lys Ile Arg Gly
335             260                 265                 270
338 Ala His Asn Tyr Ser Asn Ala Leu Ala Ala Leu Ala Leu Gly His Ala
339             275                 280                 285
342 Val Gly Leu Pro Phe Asp Ala Met Leu Gly Ala Leu Lys Ala Phe Ser
343     290                 295                 300
346 Gly Leu Ala His Arg Cys Gln Trp Val Arg Glu Arg Gln Gly Val Ser
347 305                 310                 315                 320
350 Tyr Tyr Asp Asp Ser Lys Ala Thr Asn Val Gly Ala Ala Leu Ala Ala
351             325                 330                 335
354 Ile Glu Gly Leu Gly Ala Asp Ile Asp Gly Lys Leu Val Leu Leu Ala
355             340                 345                 350
358 Gly Gly Asp Gly Lys Gly Ala Asp Phe His Asp Leu Arg Glu Pro Val
359             355                 360                 365
362 Ala Arg Phe Cys Arg Ala Val Val Leu Leu Gly Arg Asp Ala Gly Leu
363     370                 375                 380
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366 Ile Ala Gln Ala Leu Gly Asn Ala Val Pro Leu Val Arg Val Ala Thr
367 385                 390                 395                 400
370 Leu Asp Glu Ala Val Arg Gln Ala Ala Glu Leu Ala Arg Glu Gly Asp
371                 405                 410                 415
374 Ala Val Leu Leu Ser Pro Ala Cys Ala Ser Leu Asp Met Phe Lys Asn
375                 420                 425                 430
378 Phe Glu Glu Arg Gly Arg Leu Phe Ala Lys Ala Val Glu Glu Leu Ala
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383 <211> LENGTH: 449
384 <212> TYPE: PRT
385 <213> ORGANISM: Staphylococcus aureus
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393 Leu Ala Lys Ser Gly Tyr Glu Ala Ala Lys Leu Leu Ser Lys Leu Gly
394             20                  25                  30
397 Ala Asn Val Thr Val Asn Asp Gly Lys Asp Leu Ser Gln Asp Ala His
398             35                  40                  45
401 Ala Lys Asp Leu Glu Ser Met Gly Ile Ser Val Val Ser Gly Ser His
402     50                  55                  60
405 Pro Leu Thr Leu Leu Asp Asn Asn Pro Ile Ile Val Lys Asn Pro Gly
406 65                  70                  75                  80
409 Ile Pro Tyr Thr Val Ser Ile Ile Asp Glu Ala Val Lys Arg Gly Leu
410             85                  90                  95
413 Lys Ile Leu Thr Glu Val Glu Leu Ser Tyr Leu Ile Ser Glu Ala Pro
414             100                 105                 110
417 Ile Ile Ala Val Thr Gly Thr Asn Gly Lys Thr Thr Val Thr Ser Leu
418             115                 120                 125
421 Ile Gly Asp Met Phe Lys Lys Ser Arg Leu Thr Gly Arg Leu Ser Gly
422     130                 135                 140
425 Asn Ile Gly Tyr Val Ala Ser Lys Val Ala Gln Glu Val Lys Pro Thr
426 145                 150                 155                 160
429 Asp Tyr Leu Val Thr Glu Leu Ser Ser Phe Gln Leu Leu Gly Ile Glu
430             165                 170                 175
433 Lys Tyr Lys Pro His Ile Ala Ile Ile Thr Asn Ile Tyr Ser Ala His
434             180                 185                 190
437 Leu Asp Tyr His Glu Asn Leu Glu Asn Tyr Gln Asn Ala Lys Lys Gln
438             195                 200                 205
441 Ile Tyr Lys Asn Gln Thr Glu Glu Asp Tyr Leu Ile Cys Asn Tyr His
442     210                 215                 220
445 Gln Arg Gln Val Ile Glu Ser Glu Glu Leu Lys Ala Lys Thr Leu Tyr
446 225                 230                 235                 240
449 Phe Ser Thr Gln Gln Glu Val Asp Gly Ile Tyr Ile Lys Asp Gly Phe
450             245                 250                 255
453 Ile Val Tyr Lys Gly Val Arg Ile Ile Asn Thr Glu Asp Leu Val Leu
454             260                 265                 270
457 Pro Gly Glu His Asn Leu Glu Asn Ile Leu Ala Ala Val Leu Ala Cys
458             275                 280                 285
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VERIFICATION SUMMARY   DATE: 10/06/2006
PATENT APPLICATION: **US/10/531,844A**   TIME: 10:30:23

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Output Set: **N:\CRF4\10062006\J531844A.raw**

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date